

BASE COUNT 153 a 109 c 160 g 129 t
ORIGIN

Query Match

100.0%; Score 551; DB 6; Length 551;
Best local similarity 100.0%; Pred. No. 1.8e-152;

Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TTGGGATGATCTAATCAATGCAAAAGTTATCTCCAGACACGAGTTTGTGAGT 120
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QY 181 CAGAGGTTTCATCAGCTTCGGAATTTGACCTAGAGAAAAGAGTTGCCGAGAGACT 240
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DB 421 GAGCGGCGCATGTCATCAGCGTATGAGATCAATCAATGATGATTTAGTCAAG 480
QY 481 TTCAGTTGTGAG 540
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QY 541 GAGCTACAGG 551
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RESULT 2
LOCUS AT011639 1411 bp mRNA linear PLN 30-SEP-1999
DEFINITION Arabidopsis thaliana (ecotype Landsberg erecta) mRNA for squamosa promoter binding protein-like 9.
ACCESSION AJ011639
VERSION AJ011639.1 GI:5931674
KEYWORDS SPL9 gene; squamosa promoter binding protein-like 9.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1411)
AUTHORS Cardon,G.H., Hohmann,S., Nettesheim,K., Saedler,H. and Huijser,P.
TITLE Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a novel gene involved in the floral transition
JOURNAL Plant J 12 (2), 367-377 (1997)
MEDLINE 97445501
REFERENCE 2 (bases 1 to 1411)
AUTHORS Cardon,G., Hohmann,S., Klein,J., Nettesheim,K., Saedler,H. and Huijser,P.
TITLE Molecular characterisation of the Arabidopsis SBP-box genes
JOURNAL Gene 237 (1), 91-104 (1999)

MEDLINE 99453765
REFERENCE 3 (bases 1 to 1411)
AUTHORS Cardon,G.H.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-1998) Cardon G.H., Molecular Plant Genetics, Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, D-50829, GERMANY
FEATURES
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BASE COUNT 447 a 290 c 325 g 349 t
ORIGIN

Query Match
Best local similarity 99.7%; Score 549.4; DB 8; Length 1411;
Matches 550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCTGTCCTGAGAGCGGGTCCGGTCACTGAGTCAATACCAAGTCCCAAGTGAAG 60
DB 212 ACCTGTCCTGAGAGCGGGTCCGGTCACTGAGTCAATACCAAGTCCCAAGTGAAG 271
QY 61 TTGGGATGATCTAATCAATGCAAAAGTTATCTCCAGACACGAGTTTGTGAGT 120
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2002, 23:07:58 ; Search time 2022.28 Seconds

(Without alignments)
5701.743 Million cell updates/sec

Title: US-09-839-185-1

Perfect score: 1 ACGTCTCCGTGAGCGCGGT.....TAACTAGAGACTACAGG 551

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

GenBml:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

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31: em_hcg_inv:*

32: em_hcg_other:*

33: em_higo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	277.8	50.4	3180	8	ATRH011640	AJ011640 Arabidops
6	277.8	50.4	55988	8	AC002561	AC002561 Arabidops
7	160.6	29.1	1072	8	AMA011622	AJ011622 Antirrhin
8	144	26.1	1223	8	AMA011623	AJ011623 Antirrhin
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17	103	18.7	1298	8	ATRH011637	AJ011637 Arabidops
18	103	18.7	1520	8	AY070106	AY070106 Arabidops
19	103	18.7	2716	8	AY074853	AY074853 Arabidops
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25	98.8	17.9	1669	8	ATRH011625	AJ011625 Arabidops
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27	98.4	17.9	1352	8	RICRMSOA	U34039 Oryza sativ
28	97.4	17.7	1137	8	ATRH011642	AJ011642 Arabidops
29	96	17.4	2951	8	ATRH132096	AJ133096 Arabidops
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ALIGNMENTS

RESULT 1

AX024556 551 bp DNA linear PAT 15-SEP-2000

LOCUS AX024556

DEFINITION Sequence 1 from Patent WO0024914.

ACCESSION AX024556

VERSION AX024556.1 GI:10184713

KEYWORDS

SOURCE

ORGANISM

thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1 (bases 1 to 551)
de Vries, S.C., Hecht, V.F. and Schmid, E.D.,
Apomixis conferred by expression of serk interacting proteins
Patent: WO 0024914-A1 04-MAR-2000;
NOVARTIS ERINDUNGEN (AT) ; NOVARTIS AG (CH) ; HECHT VALERIE FRANCE
GABRIELLE (NL) ; SCHMIDT EDUARD DANIEL LEENDERT (NL) ; VRIES SAPE
CORNELIS DE (NL)

FEATURES

source location/Qualifiers

1..551

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"